

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/560,269  
Source: IFWP  
Date Processed by STIC: 12/20/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

## Raw Sequence Listing Error Summary

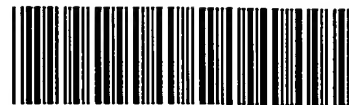
### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 10/560,269

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length     The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII     The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5   ✓   Variable Length     Sequence(s)   1   contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)           . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7      Skipped Sequences  
    (OLD RULES)     Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    (i)     SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    This sequence is intentionally skipped  
  
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)     Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
    <210> sequence id number  
    <400> sequence id number  
    000
- 9      Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>     Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n/Xaa     "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWP

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/560,269

DATE: 12/20/2005

TIME: 11:19:31

Input Set : A:\Sequence.ST25.txt

Output Set: N:\CRF4\12202005\J560269.raw

3 <110> APPLICANT: Segura, Dorotea Raventos  
4 Mygind, Per Holse  
5 Hogenhaug, Hans-Henrik Kristensen  
6 Tossi, Alessandro  
8 <120> TITLE OF INVENTION: Antimicrobial Peptides  
10 <130> FILE REFERENCE: 10496.204-US  
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/560,269  
C--> 12 <141> CURRENT FILING DATE: 2005-12-09  
12 <160> NUMBER OF SEQ ID NOS: 52  
14 <170> SOFTWARE: PatentIn version 3.3

Does Not Comply  
Corrected Diskette Needed

## ERRORED SEQUENCES

1023 <210> SEQ ID NO: 52  
1024 <211> LENGTH: 19  
1025 <212> TYPE: DNA  
1026 <213> ORGANISM: Artificial  
1028 <220> FEATURE:  
1029 <223> OTHER INFORMATION: Primer 4 sequence  
1031 <400> SEQUENCE: 52  
1032 accgtagttg cgcccatcg  
E--> 1038 ①

delete

(see p. 2 for more errors)

pat-3

19

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2

<220>  
<221> MISC\_FEATURE  
<222> (18)..(18)  
<223> Xaa = Z or Z-arginine-tryptophane-leucine wherein Z =  
phenylalanine, leucine, arginine, alanine, glycine, valine,  
tyrosine, cysteine or proline

OK, since it's explained

variable length  
not permitted.  
see item 5

<400> 1

Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
1 5 10 15

on Enon  
summary sheet

Xaa Xaa

↓  
Xaa cannot represent  
more than one amino  
acid

see p.3

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<210> 1  
<211> 18  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic antimicrobial polypeptide

<220>  
<221> MISC\_FEATURE  
<222> (2)..(2)  
<223> Xaa = leucine, isoleucine, tryptophan or methionine

tryptophan

<220>  
<221> MISC\_FEATURE  
<222> (3)..(3)  
<223> Xaa = leucine, phenylalanine, tryptophan or valine

tryptophan

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/560,269

DATE: 12/20/2005

TIME: 11:19:32

Input Set : A:\Sequence.ST25.txt

Output Set: N:\CRF4\12202005\J560269.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:124 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0

L:128 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:16

L:1038 M:254 E: No. of Bases conflict, this line has no nucleotides.